



1/12

SEQUENCE LISTING

<110> Sahni, Girish
Kumar, Rajesh
Roy, Chaiti
Rajagopal, Kammara
Nihalani, Deepak
Sundaram, Vasudha
Yadav, Mahavir

<120> NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID PROTEINS

<130> 07064/009001

<140> US 09/471,349
<141> 1999-12-23

<150> IN 3825/DEL/98
<151> 1998-12-24

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> DNA
<213> *Streptococcus equisimilis*

<220>
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<222> (1)...(1242)

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att agt ctt aaa ttt ttt gaa atc gat cta aca tca cga cct gct cat 144
 Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His
 35 40 45

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gga gga aag aca gag caa ggc tta agt cca aaa tca aaa cca ttt gct 192
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala
      50          55          60

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act gat agt ggc gcg atg tca cat aaa ctt gag aaa gct gac tta cta 240
 Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu
 65 70 75 80

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aag gct att caa gaa caa ttg atc gct aac gtc cac agt aac gac gac 288
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp
85          90          95

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tac ttt gag gtc att gat ttt gca agc gat gca acc att act gat cga Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg 100 105 110	336
aac ggc aag gtc tac ttt gct gac aaa gat ggt tcg gta acc ttg ccg Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro 115 120 125	384
acc caa cct gtc caa gaa ttt ttg cta agc gga cat gtg cgc gtt aga Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg 130 135 140	432
cca tat aaa gaa aaa cca ata caa aac caa gcg aaa tct gtt gat gtg Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val 145 150 155 160	480
gaa tat act gta cag ttt act ccc tta aac cct gat gac gat ttc aga Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg 165 170 175	528
cca ggt ctc aaa gat act aag cta ttg aaa aca cta gct atc ggt gac Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp 180 185 190	576
acc atc aca tct caa gaa tta cta gct caa gca caa agc att tta aac Thr Ile Thr Ser Gln Glu Leu Ala Gln Ala Gln Ser Ile Leu Asn 195 200 205	624
aaa aac cac cca ggc tat acg att tat gaa cgt gac tcc tca atc gtc Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val 210 215 220	672
act cat gac aat gac att ttc cgt acg att tta cca atg gat caa gag Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu 225 230 235 240	720
ttt act tac cgt gtt aaa aat cgg gaa caa gct tat agg atc aat aaa Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys 245 250 255	768
aaa tct ggt ctg aat gaa gaa ata aac aac act gac ctg atc tct gag Lys Ser Gly Leu Asn Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu 260 265 270	816
aaa tat tac gtc ctt aaa aaa ggg gaa aag ccg tat gat ccc ttt gat Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp 275 280 285	864
cgc agt cac ttg aaa ctg ttc acc atc aaa tac gtt gat gtc gat acc Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr 290 295 300	912
aac gaa ttg cta aaa agt gag cag ctc tta aca gct agc gaa cgt aac Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn 305 310 315 320	960
tta gac ttc aga gat tta tac gat cct cgt gat aag gct aaa cta ctc Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu 325 330 335	1008

tac aac aat ctc gat gct ttt ggt att atg gac tat acc tta act gga	1056
Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly	
340 345 350	
aaa gta gag gat aat cac gat gac acc aac cgt atc ata acc gtt tat	1104
Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr	
355 360 365	
atg ggc aag cga ccc gaa gga gag aat gct agc tat cat tta gcc tat	1152
Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr	
370 375 380	
gat aaa gat cgt tat acc gaa gaa gaa cga gaa gtt tac agc tac ctg	1200
Asp Lys Asp Arg Tyr Thr Glu Glu Glu Arg Glu Val Tyr Ser Tyr Leu	
385 390 395 400	
cgt tat aca ggg aca cct ata cct gat aac cct aac gac aaa	1242
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Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His	
35 40 45	
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala	
50 55 60	
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu	
65 70 75 80	
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp	
85 90 95	
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg	
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Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro	
115 120 125	
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg	
130 135 140	
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val	
145 150 155 160	
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg	
165 170 175	
Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp	
180 185 190	
Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn	
195 200 205	
Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val	
210 215 220	
Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu	
225 230 235 240	
Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys	
245 250 255	
Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu	
260 265 270	

Lys	Tyr	Tyr	Val	Leu	Lys	Lys	Gly	Glu	Lys	Pro	Tyr	Asp	Pro	Phe	Asp
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Arg	Ser	His	Leu	Lys	Leu	Phe	Thr	Ile	Lys	Tyr	Val	Asp	Val	Asp	Thr
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Asn	Glu	Leu	Leu	Lys	Ser	Glu	Gln	Leu	Leu	Thr	Ala	Ser	Glu	Arg	Asn
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Leu	Asp	Phe	Arg	Asp	Leu	Tyr	Asp	Pro	Arg	Asp	Lys	Ala	Lys	Leu	Leu
				325				330					335		
Tyr	Asn	Asn	Leu	Asp	Ala	Phe	Gly	Ile	Met	Asp	Tyr	Thr	Leu	Thr	Gly
				340			345						350		
Lys	Val	Glu	Asp	Asn	His	Asp	Asp	Thr	Asn	Arg	Ile	Ile	Thr	Val	Tyr
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Met	Gly	Lys	Arg	Pro	Glu	Gly	Glu	Asn	Ala	Ser	Tyr	His	Leu	Ala	Tyr
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Asp	Lys	Asp	Arg	Tyr	Thr	Glu	Glu	Glu	Arg	Glu	Val	Tyr	Ser	Tyr	Leu
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<212> DNA
<213> *Homo sapiens*

<220>
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<222> (1)...(777)

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gaa tgg acc tgc aag ccc ata gct gag aag tgg ttt gat cat gct gct	480
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala	
145 150 155 160	
ggg act tcc tat gtc gga gaa acg tgg gag aag ccc tac caa ggc	528
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly	
165 170 175	
tgg atg atg gta gat tgg act tgc ctg gga gaa ggc agc gga cgc atc	576
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile	
180 185 190	
act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc	624
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser	
195 200 205	
tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg	672
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu	
210 215 220	
ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag	720
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu	
225 230 235 240	
agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc	768
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gat gtt cgt	777
Asp Val Arg	

<210> 4
<211> 259
<212> PRT
<213> Homo sapiens

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35 40 45
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu
50 55 60
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr
65 70 75 80
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly
85 90 95
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu
100 105 110
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu
115 120 125
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly
130 135 140

Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala
 145 150 155 160
 Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly
 165 170 175
 Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile
 180 185 190
 Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser
 195 200 205
 Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu
 210 215 220
 Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu
 225 230 235 240
 Arg His Thr Ser Val Gln Thr Ser Ser Gly Ser Gly Pro Phe Thr
 245 250 255
 Asp Val Arg

<210> 5
 <211> 1377
 <212> DNA
 <213> Streptococcus equisimilis

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 caattgggtt ttagcgttgc tggactgtt gaggggacga atcaagacat tagtcttaaa 240
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 caagaattac tagctcaagc acaaaggattt ttaaacaaaaa accacccagg ctatacgatt 780
 tatgaacgtt actccctcaat cgtcactcat gacaatgaca tttccgtac gatttacca 840
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 aatctggtc tgaatgaaga aataaacaac actgacacttgc tctctgagaa atattacgtc 960
 cttaaaaaaag gggaaaagcc gtatgtccc ttgtatcgat gtcacttgcgacttgcacc 1020
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 aatcacgtt acaccaaccg tattataacc gtttatatgg gcaagcgacc cgaaggagag 1260
 aatgctatcgat atcattatcgat tattataacc gatcgatataa ccgaagaaga acgagaagtt 1320
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<210> 6
 <211> 1327
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

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 aaataacagc caattgggtt ttagcgttgc tggactgtt gaggggacga atcaagacat 180
 tagtcttaaa tttttgaaa tcgatctaactc acacgaccc gctcatggag gaaagacaga 240
 gcaaggcttca agtccaaat caaaaccatt tgctactgtt agtggcgcga tgcacataa 300
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taacgacgac	tactttggg	tcattgattt	tgcaagcgat	gcaaccatta	ctgatcgaaa	420
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agaattttg	ctaagccgac	atgtgcgcgt	tagaccatat	aaagaaaaac	caatacaaaa	540
ccaagcgaaa	tctgttgatg	tggaatatac	tgtacagttt	actcccttaa	accctgatga	600
cgatttcaga	ccaggtctca	aagatactaa	gctattgaaa	acactagcta	tcggtgacac	660
catcacatct	caagaattac	tagctcaagc	acaaggcatt	ttaaacaaaa	accacccagg	720
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taaactactc	tacaacaatc	tcgatgttt	tggtattatg	gactatacct	taactggaaa	1140
agtagaggat	aatcaccgtg	acaccaacgg	tatcataacc	gtttatatgg	gcaagcgacc	1200
cgaaggagag	aatgctagct	atcatttagc	ctatgataaa	gatcggtata	ccgaaagaaga	1260
acgagaagt	tacagctacc	tgcgttatac	aggacacct	atacctgata	accctaacga	1320
caaataa						1327

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<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<221> CDS

<222> (2)...(52)

<400> 7

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49

ccc

Pro

52

<210> 8

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated protein

<400> 8

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Pro

<210> 9

<211> 1541

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

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gaaagacaga	gcaaggctt	agtccaaaat	caaaaccatt	tgctactgat	agtggcgca	240
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<210> 10

<211> 1661

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 10

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agaccacaac gtttccctc tagaaataat ttgtttaac ttaagaagg agatataccca
tgattgtgg acctgagtgg ctgctagacc gtccatctgt caacaacagc caattgggtg
ttagcgttgc tggtaactgtt gaggggacga atcaagacat tagtctaaa tttttgaaa
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tcattgattt tgcaaggcgt gcaaccatta ctgatcgaaa cggcaaggc
acaaagatgg ttcggttaacc ttgcccaccc aacctgtcca agaatttttgc
atgtgcgcgt tagaccatat aaagaaaaac caatacaaaa ccaagcgaaa
tggaaataac tgtaactgtt actcccttaa accctgtatga cgatttcaga
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tagctcaagc acaaaggatt taaaacaaaa accaccagg ctatacgatt
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tgaagaaga aataaaaaac actgacccgt tctctgagaa atattacgtc
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tcgatgttt tggtaattatg gactatacct taactggaaa agtagaggat
acaccaacgg tatcataacc gtttatatgg gcaagcgacc cgaaggagag
atcatttagc cgggtgggtt caggcgcagc aatggttca gccccagtc
tcagtcaaag caagcccggt tggtatgaca atggaaaaca ctatcgata
qqqaqcqgac ctacctaggt aatgtgttgg ttgtacttq ttatggagga

ttaactgcga aagttaaacct	gaagctgaag	agacttgctt	tgacaagtagc	actggaaaca	1560
cttaccgagt	gggtgacact	tatgagcgtc	ctaaagactc	catgatctgg	1620
gcatcgggc	tggcgaggg	agaataagct	gtaccatcta	a	1661

<210> 11

<211> 1782

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 11

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acgctgccc	agatctcgat	cccgcaaat	taatacgact	cactataggg	agaccacaac	180
ggttccctc	tagaaataat	tttgcgttaac	ttaagaagg	agatatacc	tggtgcaagc	240
acaacagatt	gtaccatag	ctgagaagt	ttttgatcat	gctgctgg	cttcctatgt	300
ggtcggagaa	acgtgggaga	aggcagcga	cgcatcaact	gcacttctag	aaatagatgc	360
aacgatcagg	acacaaggac	atcctataga	attggagaca	cctggagca	gaaggataat	420
cgaggaaacc	tgctccatg	catctgcaca	ggcaacggc	gaggagatg	gaagtgtgag	480
agcaccac	ctgtgcagac	cacatcgagc	ggatctggc	ccttcaccc	tgtctgtatt	540
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ccatttgcta	ctgatagtgg	cgcgtatgc	cataaaactt	agaaagctga	cttactaaag	780
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<220>

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